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QY 1561 TCIGTCATCCCTTGTGCAACIAATAAATACATCTTCGATTCAGAGGCGCTTCCTCC 1620
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QY 1681 TTTTAGTGCACCCCAAGGCGGCGCTTAATTTCTGCTTGGTTCGAATATCTTCAT 1740
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DB 1942 GATTGGAAGCATCGCATCATATATTAATGCTGATTTATGATCTCGCAATTCGAAGCA 2001
QY 1801 TCACTAACACAGGAAAAATAC 1822
DB 2002 TCACTAACACAGGAAAAATAC 2023

RESULT 2
AX328009 3768 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 4 from Patent WO0190146.
ACCESSION AX328009
VERSION AX328009.1 GI:18098152
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catartini; Hominidae; Homo.
1
Curtis,R.A.
5256 and 5289, human transporters and uses thereof
Patent: W0 0190146-A 1 29-NOV 2001.
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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/note="unnamed protein product"
/codon_start=1
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QNLGAMSSYFLIKYELPEVIRAPMSLENTGEXLNGNYLTFVSGYLLPSLKN
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ALPTILVAFVCHPEVLPILSELKDSERKQIVNSITGMVIMVILLALPGLTFYCG
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BASE COUNT 1156 a 712 c 691 g 1209 t
CIG:N

Query Match
Best local Similarity 96.43; Score 1793.6; DB 6; Length 3768;
Matches 17%; Conserved: 6; Mismatches 4; Indels 0; Gaps 0;

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DB 18 CCGTCGACAGCATGGATATAAATTAAGAACAGAGTGTTCIGCAATATCAACACAAAGTG 77
QY 83 GAAGAACCTTAAGCTGAAGGTACAGTATATTATACACTGAAGGCGCTTGTGTGTGAGAC 142
DB 78 GAAGAACCTTAAGCTGAAGGTACAGTATATTATACACTGAAGGCGCTTGTGTGTGAGAC 137
QY 143 AAGAAAGCGCTTGAAGCTCAAAAGCATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 202

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DB 138 AAGAAAGCGCTTGAAGCTCAAAAGCATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 197
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DB 198 GATGCAACAGCATGGATATAAATTAAGAACAGAGTGTTCIGCAATATCAACACAAAGTG 257
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DB 258 GATGCAACAGCATGGATATAAATTAAGAACAGAGTGTTCIGCAATATCAACACAAAGTG 317
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DB 1038 GATGCAACAGCATGGATATAAATTAAGAACAGAGTGTTCIGCAATATCAACACAAAGTG 1097
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RESULT 13
AX392946
LOCUS
DEFINITION Sequence 48 from Patent WO0212340.
ACCESSION AX392946
VERSION AX392946.1 GI:19700993
KEYWORDS
SOURCE
ORGANISM human.
REFERENCE
AUTHORS
Yue, H., Thornton, M., Parkumai, J., Tang, Y., Li, P., Wang, Y.,
Baughn, M.R., Yang, J., Yao, M.G., Lal, P., Wallia, N.K., Gandhi, A.R.,
Batalla, A.T., Nguyen, D.B., Patterson, C., Elliott, V.S.,
Tribouley, C.M., Lu, D.A., Xu, Y., Peddy, R., Bernabucci, R.,
Borowsky, W., Le, P., Li, Y., Pollock, D., Greene, B.D.,
Sanjanwalla, M.S., Raimano, B.E., Barford, N., Isom, C.H., Lee, E.A.,
Ding, L., Das, D., Pollock, D.A., Rhoads, P.A., and Seifhamer, J.J.
Patent: WO/0213149 A 48 14 FEB 2002.
JOURNAL
FEATURES
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Location/Qualifiers
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DB_xref: "taxon:6062"
/feature: "nucleotide ID NO. 7460846CB1"
BASE COUNT 582 a 486 c 482 g 770 t
Query Match 27.8%, Score 556.6, DB 6, Length 2420;
Best Local Similarity 60.1%, Pred. No. 2.2e-123;

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 08:33:36 ; Search time 1293.47 Seconds
(without alignments)
11249.881 Million cell updates/sec

Title: US-09-776-705-3_COPY_1_500

Perfect score: 500

Sequence: 1 agcttagcaaatatgatgcac.....ataatgcacaaataaactgaa 500

Scoring table: IDENTITY_NUC

Gapex 10.0 , Gapext 1.0

Searched: 251640 seqs, 1155,100,078 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2777777

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: GenBank

2: gb_pat

3: gb_inv

4: gb_em

5: gb_ov

6: gb_pat

7: gb_inv

8: gb_em

9: gb_ov

10: gb_pat

11: gb_inv

12: gb_em

13: gb_ov

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15: gb_inv

16: gb_em

17: gb_ov

18: gb_pat

19: gb_inv

20: gb_em

21: gb_ov

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23: gb_inv

24: gb_em

25: gb_ov

26: gb_pat

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29: gb_ov

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31: gb_inv

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34: gb_pat

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36: gb_em

37: gb_ov

38: gb_pat

39: gb_inv

40: gb_em

41: gb_ov

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	500	100.0	37921	9	AC005854 Homo sapi
2	500	100.0	37921	9	AC005854 Homo sapi
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ALIGNMENTS

RESULT 1	AC005854/c	AC005854	37921 bp	DNA	110000	PREL 40-MAR-1999
LOCUS	AC005854/c	Homo sapiens, complete sequence				
DEFINITION	AC005854	Homo sapiens, complete sequence				
ACCESSION	AC005854	Homo sapiens, complete sequence				
VERSION	AC005854.2	GI:4454568				
KEYWORDS	HLA					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1	GenBank				
AUTHORS	1	GenBank				
TITLE	1	GenBank				
JOURNAL	1	GenBank				

Pred. No. is the number of results predicted by chance to have a


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* 20367 20366: gap of 100 bp
* 20367 21057: contig of 691 bp in length
* 21058 21157: gap of 100 bp
* 21158 21822: contig of 665 bp in length
* 21823 21922: gap of 100 bp
* 21923 22691: contig of 769 bp in length
* 22692 23463: contig of 772 bp in length
* 23464 24221: contig of 757 bp in length
* 24222 24321: gap of 100 bp
* 24322 25050: contig of 688 bp in length
* 25051 25150: gap of 100 bp
* 25151 25667: contig of 717 bp in length
* 25668 26667: contig of 700 bp in length
* 26668 27457: contig of 630 bp in length
* 27458 27557: gap of 100 bp
* 27558 28268: contig of 711 bp in length
* 28269 29047: gap of 100 bp
* 29048 29147: gap of 100 bp
* 29148 29856: contig of 709 bp in length
* 29857 30655: contig of 699 bp in length
* 30656 31451: contig of 636 bp in length
* 31452 32243: contig of 632 bp in length
* 32244 33010: contig of 767 bp in length
* 33011 33790: contig of 680 bp in length
* 33791 34569: contig of 679 bp in length
* 34570 35360: contig of 691 bp in length
* 35361 36160: contig of 700 bp in length
* 36161 36964: contig of 704 bp in length
* 36965 37789: contig of 725 bp in length
* 37790 38567: contig of 678 bp in length
* 38568 39366: contig of 699 bp in length
* 39367 40137: contig of 671 bp in length
* 40138 40904: contig of 567 bp in length
* 40905 41684: contig of 680 bp in length
* 41685 42490: contig of 706 bp in length
* 42491 43290: gap of 100 bp
* 43291 44085: contig of 765 bp in length
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* 44864 45667: contig of 704 bp in length
* 45668 46478: contig of 711 bp in length
* 46479 47281: contig of 703 bp in length
* 47282 48081: gap of 100 bp
* 48082 48883: contig of 662 bp in length
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QY 233 TTCTCAATTCCTCAGAACCATGATAAATATATCTATATAAGAAATTAAGAGCTCAGACACA 292
DB 7833 TTAATAAACAAGATGATATAAATATTAACACTTATTCATTAATAAATAAAGATCATAACAA 7892
QY 292 TCATAGAACCTTGAAGACGACAAATTTTCTTCAA:ATCTTCAA:AAATGATGTCATC 352
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QY 413 ACTCAGAAATTCATTTACAGACATAGCTCATTGTGTGAAAAAAGTTATTCAGGCA 470
DB 8013 TTTTCAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8070

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ACCESSION AX251504
VERSION AX251504.1 GI:15984927
KEYWORDS
SOURCE synthetic construct,
synthetic construct,
artificial sequences,
bases 1 to 46342
REFERENCE Olek, A., Piepenbrock, C. and Berlin, K.
AUTHORS
TITLE Diagnosis of diseases associated with tumor suppressor genes and
JOURNAL Epigenomics AG (DE)
FEATURES
Location/Qualifiers
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ZBBBBSB "taxon:32630"
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ACCESSION AX344503
VERSION AX344503.1 GI:18452391
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SOURCE synthetic construct,
synthetic construct,
artificial sequences,
bases 1 to 38342
REFERENCE Olek, A., Piepenbrock, C. and Berlin, K.
AUTHORS
TITLE Diagnosis of diseases associated with signal transduction
JOURNAL Epigenomics AG (DE)
FEATURES
Location/Qualifiers
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ZBBBBSB "taxon:32630"
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Matches 184; Conservative 0; Mismatches 206; Indels 4; Gaps 1;

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DB 2345 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2246
QY 96 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 155
DB 23285 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 22246
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 09:33:36, Search time 1296.06 seconds
(without alignments)
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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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C 40	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 41	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 42	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 43	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 44	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 45	45.8	9.1	14924	6	AX281156	AX281156 Sequence

REFERENCES

Result No.	Score	% Match	Query Length	DB Length	DB ID	Description
C 1	501	100.0	37921	9	AC005854	AC005854 Homo sapi
C 2	430	67.8	167539	9	AC008014	AC008014 Homo sapi
C 3	430	67.8	244100	6	AC0080136	AC0080136 Homo sapi
C 4	52.6	10.5	11049	6	AX281156	AX281156 Sequence
C 5	52.6	10.5	11049	6	AX445670	AX445670 Sequence
C 6	52.6	10.5	11049	6	AX445670	AX445670 Sequence
C 7	52.6	10.5	11049	6	AX445670	AX445670 Sequence
C 8	52.6	10.5	11049	6	AX445670	AX445670 Sequence
C 9	51.6	10.3	191503	9	AC094803	AC094803 Homo sapi
C 10	50	10.0	10176	3	AF001370	AF001370 Homo sapi
C 11	50	10.0	145430	2	AL845421	AL845421 Homo sapi
C 12	50	10.0	244114	5	AL005633	AL005633 Homo sapi
C 13	49.4	9.9	2212	3	ME117089	ME117089 Homo sapi
C 14	49.4	9.9	104434	3	AC117089	AC117089 Homo sapi
C 15	49.4	9.9	110500	2	AC117089	AC117089 Homo sapi
C 16	49.4	9.9	25117	2	AC117089	AC117089 Homo sapi
C 17	49.4	9.9	192319	2	AL845439	AL845439 Homo sapi
C 18	49	9.8	112124	5	AL116102	AL116102 Homo sapi
C 19	48.4	9.7	44996	3	AC094809	AC094809 Homo sapi
C 20	48.4	9.7	162214	9	AL353741	AL353741 Homo sapi
C 21	48.4	9.7	192517	9	AL353741	AL353741 Homo sapi
C 22	48.4	9.7	192517	9	AL353741	AL353741 Homo sapi
C 23	48.4	9.7	192517	9	AL353741	AL353741 Homo sapi
C 24	48	9.6	118001	5	AC073081	AC073081 Homo sapi
C 25	47.4	9.5	157320	2	AC118889	AC118889 Homo sapi
C 26	47.4	9.5	188561	10	AL353741	AL353741 Homo sapi
C 27	47.4	9.5	188561	10	AL353741	AL353741 Homo sapi
C 28	47.4	9.5	188561	10	AL353741	AL353741 Homo sapi
C 29	47.4	9.5	188561	10	AL353741	AL353741 Homo sapi
C 30	46.6	9.3	143501	2	AC116936	AC116936 Homo sapi
C 31	46.6	9.3	143501	2	AC116936	AC116936 Homo sapi
C 32	46.2	9.2	145514	2	AC006872	AC006872 Homo sapi
C 33	46.2	9.2	145514	2	AC006872	AC006872 Homo sapi
C 34	46.2	9.2	145514	2	AC006872	AC006872 Homo sapi
C 35	46.2	9.2	145514	2	AC006872	AC006872 Homo sapi
C 36	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 37	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 38	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 39	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 40	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 41	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 42	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 43	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 44	45.8	9.1	14924	6	AX281156	AX281156 Sequence
C 45	45.8	9.1	14924	6	AX281156	AX281156 Sequence

Pred. No. is the number of results predicted by chance to have a

[illegible]

[illegible]

Next, this sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., filtered quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

repeat_region	14317..14429	/rpt_family="L1"
repeat_region	14424..14446	/rpt_family="AT_rich"
repeat_region	14761..14780	/rpt_family="L2"
repeat_region	15858..16070	/rpt_family="(TAAA)n"
repeat_region	16092..16121	/rpt_family="L2"
repeat_region	16132..16413	/rpt_family="(TTTA)n"
repeat_region	17001..17265	/rpt_family="Alu"
repeat_region	18228..18354	/rpt_family="MaLR"
repeat_region	19376..19524	/rpt_family="MIR"
repeat_region	19688..20131	/rpt_family="MaLR"
repeat_region	21251..21272	/rpt_family="ERV1"
repeat_region	21519..21745	/rpt_family="(IG)n"
repeat_region	21727..21759	/rpt_family="Alu"
repeat_region	22840..22772	/rpt_family="AT_rich"
repeat_region	23379..23493	/rpt_family="MaLR"
repeat_region	23475..23509	/rpt_family="MIR"
repeat_region	24800..25255	/rpt_family="AT_rich"
repeat_region	25322..25267	/rpt_family="L1"
repeat_region	25340..25455	/rpt_family="(TAAAA)n"
repeat_region	25399..25659	/rpt_family="MIR"
repeat_region	26216..26357	/rpt_family="AT_rich"
repeat_region	27143..27898	/rpt_family="L2"
repeat_region	28048..28103	/rpt_family="L1"
repeat_region	28111..28219	/rpt_family="L1"
repeat_region	28279..28321	/rpt_family="AT_rich"
repeat_region	28548..28934	/rpt_family="MaLR"
repeat_region	28571..28601	/rpt_family="AT_rich"
repeat_region	30595..31015	/rpt_family="(TA)n"
repeat_region	31230..31590	/rpt_family="MaLR"
repeat_region	32355..33236	/rpt_family="MaLR"
repeat_region	33235..33305	/rpt_family="(TTTAA)n"

Query Match: 10.3%; Score 51.6; DB 9; Length 178378;
Best Local Similarity 51.8%; Pred. No. 0.51;
Matches 117; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

95 TTAAGTGGCGGTGATAGCAAAAACACTGAAGGATGAGACACACATAAAGTTTCAT 154
| | | | | | | | | | | | | | | | | | | | | |
bb 117717 TAAACAGCGCTTTTAGRAAAAAAIAATTTTAACTCTCTGTGTCAACAATTGAATTTCAT 117776

95 GTAAATTGTGAGTGCTCAIITTAACACAAICTTTTGCCCAIGTGCAACAAATTAACG 214

Genome version 5.1.2
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EM nucleotide - nucleic search, using sw model

Run on: January 4, 2003, 08:33:46 : Search time 1296.06 Seconds
(without alignments)
10214.823 M.222.6 vch1 -update:sw

Title: us-09-776-705_3_COPY_30000_40500

Perfect score: 501

Sequence: 1 dataattttttataatattt.....atatattatctatctatcaaat 501

Scoring table: IDENTITY_NW
Gapop 10.0, Gapext 1.0

Searches: 2054640 seqs, 14551402978 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2009000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: GenBank

1: ab_bat.*
2: ab_bat.*
3: ab_bat.*
4: ab_bat.*
5: ab_ov.*
6: ab_pat.*
7: ab_pat.*
8: ab_pl.*
9: ab_pl.*
10: ab_ro.*
11: ab_ro.*
12: ab_ro.*
13: ab_ro.*
14: ab_ro.*
15: ab_ro.*
16: ab_ro.*
17: ab_ro.*
18: ab_ro.*
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29: ab_ro.*
30: ab_ro.*
31: ab_ro.*
32: ab_ro.*
33: ab_ro.*
34: ab_ro.*
35: ab_ro.*
36: ab_ro.*
37: ab_ro.*
38: ab_ro.*
39: ab_ro.*
40: ab_ro.*
41: ab_ro.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	II	Accession
1	5.1	100.0	6.33	9	AB055053	AB055053 Homo sapiens
2	5.1	100.0	6.33	9	AB055054	AB055054 Homo sapiens
3	5.01	100.0	16.79	9	AB055054	AB055054 Homo sapiens
4	5.01	100.0	24.11	2	AB055054	AB055054 Homo sapiens
5	4.96	97.8	9.66	9	AB055054	AB055054 Homo sapiens
6	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
7	1.95	95.3	1.87	6	AB055054	AB055054 Homo sapiens
8	1.77	95.3	1.87	6	AB055054	AB055054 Homo sapiens
9	1.55	90.9	18.90	2	AB055054	AB055054 Homo sapiens
10	5.9	100.0	14.07	2	AB055054	AB055054 Homo sapiens
11	5.72	100.0	14.07	2	AB055054	AB055054 Homo sapiens
12	5.5	100.0	14.07	2	AB055054	AB055054 Homo sapiens
13	5.5	100.0	14.07	2	AB055054	AB055054 Homo sapiens
14	5.3	100.0	14.07	2	AB055054	AB055054 Homo sapiens
15	5.3	100.0	14.07	2	AB055054	AB055054 Homo sapiens
16	5.2	100.0	14.07	2	AB055054	AB055054 Homo sapiens
17	5.2	100.0	14.07	2	AB055054	AB055054 Homo sapiens
18	5.18	100.0	14.07	2	AB055054	AB055054 Homo sapiens
19	5.12	100.0	14.07	2	AB055054	AB055054 Homo sapiens
20	5.08	100.0	14.07	2	AB055054	AB055054 Homo sapiens
21	5.08	100.0	14.07	2	AB055054	AB055054 Homo sapiens
22	5.04	100.0	14.07	2	AB055054	AB055054 Homo sapiens
23	5.02	100.0	14.07	2	AB055054	AB055054 Homo sapiens
24	5.02	100.0	14.07	2	AB055054	AB055054 Homo sapiens
25	4.96	97.8	9.66	9	AB055054	AB055054 Homo sapiens
26	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
27	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
28	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
29	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
30	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
31	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
32	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
33	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
34	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
35	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
36	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
37	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
38	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
39	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
40	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
41	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
42	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
43	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
44	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
45	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens

ALIGNMENTS

Result No.	Score	Match	Length	DB	II	Accession
1	5.1	100.0	6.33	9	AB055053	AB055053 Homo sapiens
2	5.1	100.0	6.33	9	AB055054	AB055054 Homo sapiens
3	5.01	100.0	16.79	9	AB055054	AB055054 Homo sapiens
4	5.01	100.0	24.11	2	AB055054	AB055054 Homo sapiens
5	4.96	97.8	9.66	9	AB055054	AB055054 Homo sapiens
6	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
7	1.95	95.3	1.87	6	AB055054	AB055054 Homo sapiens
8	1.77	95.3	1.87	6	AB055054	AB055054 Homo sapiens
9	1.55	90.9	18.90	2	AB055054	AB055054 Homo sapiens
10	5.9	100.0	14.07	2	AB055054	AB055054 Homo sapiens
11	5.72	100.0	14.07	2	AB055054	AB055054 Homo sapiens
12	5.5	100.0	14.07	2	AB055054	AB055054 Homo sapiens
13	5.5	100.0	14.07	2	AB055054	AB055054 Homo sapiens
14	5.3	100.0	14.07	2	AB055054	AB055054 Homo sapiens
15	5.3	100.0	14.07	2	AB055054	AB055054 Homo sapiens
16	5.2	100.0	14.07	2	AB055054	AB055054 Homo sapiens
17	5.2	100.0	14.07	2	AB055054	AB055054 Homo sapiens
18	5.18	100.0	14.07	2	AB055054	AB055054 Homo sapiens
19	5.12	100.0	14.07	2	AB055054	AB055054 Homo sapiens
20	5.08	100.0	14.07	2	AB055054	AB055054 Homo sapiens
21	5.08	100.0	14.07	2	AB055054	AB055054 Homo sapiens
22	5.04	100.0	14.07	2	AB055054	AB055054 Homo sapiens
23	5.02	100.0	14.07	2	AB055054	AB055054 Homo sapiens
24	5.02	100.0	14.07	2	AB055054	AB055054 Homo sapiens
25	4.96	97.8	9.66	9	AB055054	AB055054 Homo sapiens
26	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
27	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
28	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
29	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
30	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
31	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
32	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
33	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
34	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
35	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
36	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
37	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
38	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
39	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
40	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
41	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
42	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
43	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
44	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens
45	4.93	100.0	17.09	2	AB055054	AB055054 Homo sapiens

Matches 501; Conservative 0; Mismatches 0; Models 0; Caps 0;

[illegible]

Viola, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, T., Zemel, A., and Zody, H.

JOURNAL

COMMENT

Submitted: 12/1/2002 (2002) Whitehead Institute/MIT Center for Genome Research
 On Aug 21, 2002 this sequence version replaced g1:21591843.
 All repeats were identified using RepeatMasker:
 Smith, A. F. A. & Green, P. (1996:1997)
 http://ftp.gene.washington.edu/kb/kb/peathasket.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L20293

Center clone name: 447C-7

----- Summary Statistics

Sequencing vector: pUC19, 177096 bp

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 6.667.1

Consensus quality: 173905 bases at least Q40

Consensus quality: 175457 bases at least Q30

Insert size: 159000; agarose-gel

Insert size: 176296; sum-of-contigs

Quality coverage: 11.4 in 500 bases; average-gp

Quality coverage: 10.9 in 920 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of a contigs, gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 54559 contig of 54559 bp in length
 * 54360 54459 gap of 100 bp
 * 54460 54459 contig of 1031 bp in length
 * 55491 55590 gap of 100 bp
 * 55591 57338 contig of 1748 bp in length
 * 57339 57438 gap of 100 bp
 * 57439 60576 contig of 3138 bp in length
 * 60577 60676 gap of 100 bp
 * 60677 60676 contig of 11762 bp in length
 * 72439 72538 gap of 100 bp
 * 72439 72538 contig of 26096 bp in length
 * 92539 92734 gap of 100 bp
 * 92735 119761 contig of 27327 bp in length
 * 119762 119861 gap of 100 bp
 * 119862 161627 contig of 41066 bp in length
 * 161628 161627 gap of 100 bp
 * 161628 177096 contig of 15469 bp in length.

FEATURES

source
 1. 177096
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 /db_xref="taxon:10090"
 /clone="RP23-447G7"
 /clone_lib="RC1-23 Female Mouse BAC"

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1. 54559
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 /vector="SP6"
 /clone_side="left"

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 Direct Submission
 Published
 2 (bases 1 to 184007)
 Worley, K.C.
 Direct Submission
 Submitted (00-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 184007)
 Worley, K.C.
 Direct Submission
 Submitted (28-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 18, 2002 this sequence entry is replaced by 120514476.

 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.bcm.tmc.edu/
 Contact: hgc-help@bcm.tmc.edu

 Project Information
 Center project name: GW03
 Center clone name: CH230.2862

 Summary Statistics
 Sequencing vector: plasmid
 Chemistry: Dye-terminator Run type: 100% of reads
 Assembly program: Phrap; version 0.99c29
 Consensus quality: 100% bases at least Q40
 Consensus quality: 100% bases at least Q40
 Consensus quality: 142367 bases at least Q20

 * Note: Estimated insert size may differ from sequence length
 * Note: This is a working draft sequence. It currently
 * consists of 63 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence,
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 1057: contig of 1057 bp in length
 * 1058 1157: contig of unknown length
 * 1158 2493: contig of 1224 bp in length
 * 2481 2480: gap of unknown length



process e.g. cellular proliferation, growth, differentiation, or migration, which is useful in treatment and diagnosis of transporter associated disorders, these disorders include central nervous system (CNS) disorders, autoimmune function disorders, learning or memory disorders, bipolar affective neurological disorders, cardiac-related disorders, cancer, tumor angiogenesis and metastasis, skeletal dysplasia, hepatic disorders, haematopoietic and/or erythropoietic disorder, hormonal disorders, and immune disorders. The polypeptides and polynucleotides, and biomarkers of the polynucleotides and antibodies, are useful for screening assays, predictive medicine (e.g. diagnostic assays, prognostic assays, metabolizing clinical trials, and pharmacogenetics) and treatment (e.g. therapeutic and prophylactic).

XX Sequence 4767 BP; 1157 A; 713 C; 699 G; 1267 T; 0 other;

Query Map:
 Best Local Similarity 99.8%; Score 496.4; Pos 24; Length 4767;
 Matches 500; Overlap 0; Mismatches 11; Labels 0; Gaps 0;

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 DB 2487 AAGGAGCTTTTATTCATATGACGACACACACACACACACACACACACACACACAC 2546
 QY 121 TTCTAAGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTATACCTTTGTCAT 180
 DB 2547 TTCTAAGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTATACCTTTGTCAT 2606
 QY 181 TGAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 DB 2607 TGAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2666
 QY 241 GAGGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 2667 GAGGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 3066
 QY 301 GAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 2727 GAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2786
 QY 361 AATGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 2787 AATGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 2846
 QY 421 AATGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 2847 AATGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 2906
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 DB 2907 CATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2966

RESULT 3

AAAL21895

ID AAAL21895 standard; cDNA, 472 BP.

AC AAAL21895;

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XX 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 1452.

KW Human breast cancer; cell marker; cytostatic; ss.

XX Homo sapiens.

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XX W-200151628-A2.

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XX 19-JUL-2001.

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XX 10-JAN-2001; 2001W-0500798.

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XX 14-JAN-2001; 2000S-0176077.

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XX 14-MAR-2001; 2000S-0199177.

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XX 24-MAR-2001; 2000S-0192099.

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XX 25-MAR-2001; 2000S-0192400.

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XX 15-MAY-2000; 2000S-0205240.

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XX 09-JUN-2001; 2000S-0211315.

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XX 25-JUL-2000; 2000S-0220544.

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XX (MILL-) MILLERIN PRELIMINARY INQ.

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XX 24-JUL-01; Xu Y, Wang Y, Steinman K;

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XX WEL, 2001; 4767/48.

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XX New peptide useful as a marker for the diagnosis of breast cancer

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XX Claim 1; Page 2572; 3695pp; English.

XX

XX the invention relates to a method for assessing whether a patient is

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XX (AA10744; AA126949) and methods of assessing whether a patient is

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XX afflicted with breast cancer by examining the correlation between the

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XX expression of certain markers and the various state of breast cells.

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XX The polynucleotide 1452 and related polypeptides are potential markers for

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XX detecting, diagnosing, monitoring, characterizing treatment and

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XX potentially preventing breast cancer. The polynucleotides and encoded

XX

XX polypeptides are also useful for isolating compounds with cytostatic

XX

XX Sequence 472 BP; 157 A; 89 C; 699 G; 1267 T; 0 other;

XX

XX Query Map:
 Best Local Similarity 99.7%; Score 496.4; Pos 24; Length 472;

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XX Matches 471; Overlap 0; Mismatches 11; Labels 0; Gaps 0;

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XX 100 AATAGATTTTGTAAATGTTAAACATCTATATTTAAATGTTAAACACTAAATATAGAG 159

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XX 160 AAGGAGCTTTTATTCATATGACGACACACACACACACACACACACACACACACAC 219

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XX 121 TTCTAAGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCT 180

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XX 221 TTCTAAGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCT 280

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XX 181 TGAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

XX

XX 280 TGAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 340

XX

XX 241 GAGGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 300

XX

XX 340 GAGGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 400

XX

XX 400 GAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460

XX

XX 361 AATGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 420

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XX 460 AATGAGCAICGCTTTTCATGTTATTCCTTAAATGCTGCTGCTGCTGCTGCTGCTGCT 520

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XX 07-DEC-2001 (first entry)

XX		Human breast cancer expressed polypeptide id: 5482.
DE		
XX		Human breast cancer; cell marker; cytostatic; gsc.
KW		Human breast cancer; cell marker; cytostatic; gsc.
XX		Homo sapiens.
OS		
XX		WU20011529-A2.
IN		
PP		19-JUL-2001.
XX		
XX		10-JAN-2001; 2001WS-U350749.
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XX		14-JAN-2000; 2000US-0176077.
PR		14-MAR-2000; 2000GS-0189167.
FF		24-MAR-2000; 2000US-0192099.
PR		29-MAR-2000; 2000US-0193460.
FF		15-MAY-2000; 2000US-0205240.
PR		09-JUN-2000; 2000US-0211315.
PR		25-JUL-2000; 2000US-0220544.
XX		(Publ.) RESEARCH IN PROGRESS
XX		Lillie J., Xu Y., Wang Y., Steinmann K;
DR		WP1; 2001-451856/48.
XX		New peptide useful as a marker for the diagnosis of breast cancer -
PT		Claim 1; page 986; 4695pp; English.
XX		The invention relates to human breast cancer expressed polypeptides
PS		(AAU0744-AAU26789) and methods of assessing whether a patient is
CC		afflicted with breast cancer by examining the correlation between the
OC		expression of certain markers and the oncogenic status of breast cells
CC		The polynucleotides and encoded polypeptides are potential markers for
CC		detecting and diagnosing, monitoring, characterising treating and
CC		potentially preventing breast cancer. The polynucleotides and encoded
CC		polypeptides are also useful for isolation compounds with cytostatic
CC		activity.
XX		
XX		Sequence 456 BP: 142 A; 41 G; 71 C; 162 T; 0 other.
SQ		
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		Matches: 439; Conserved: 0; Mismatches: 0; Models: 0; Gaps:
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QY	61	AGAGCGTTTATTTCGAATCAGACATCAACAACAAAATAATGCTATATAGCTAAATGGCTG 120
DG	188	AGAGAGTTTATTTCGAATCAGACACAAATAAAGAAATAGCTATATAGCTAAATTTTGCAAT 247
QY	121	TCTCAAGAACATAGCTGTTTTTGAATTTATTTTAAAGCTTTTCTTTTGAATTTTGCAT 180
DG	249	TCTCAAGAACATAGCTGTTTTTGAATTTATTTTAAAGCTTTTCTTTTGAATTTTGCAT 307
QY	181	TCAAGAAAGCTGTCTCTGCTGCTCAAGCTGATATGAAATTTTAGAACATTAATAAT 240
DG	408	TCAATTAATGCTGTCTCTGCTGCTCAAGCTGATATGAAATTTTAGAACATTAATAAT 467
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DG	468	GTCGATATATCACTACGACTATGCTTTGATATATTTTATTTTATTTTATTCATATAAATATTCAGTCA 427
QY	301	GAAGATGTCATTTGCTATATGCTTTATGATATAAATCTTA 439
DG	428	GAAGATGTCATTTGCTATATGCTTTATGATATAAATCTTA 466
RESULT	5	

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121 AATCATTCATATGTAICGICGTA'AAAT 149

Search completed: January 4, 2003, 12:30:47
Job time : 767.955 secs

[illegible]

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10 72 ATGCTGAGCTTTCTTCTTCTGTCACCTGAGGCTCTCCATATACAGGAGCTTAAA 131
 QY 1235 GATCGGTCGACAGAAAAATGAAAGGAGGCTGAAATATTTGATGAGGATGCTTC 1294
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 QY 1295 ATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464
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 10 192 AGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
 QY 1455 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1414
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 252 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 111
 QY 1415 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1474
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 412 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
 QY 1475 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1544
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 472 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
 QY 1535 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1594
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 432 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
 QY 1595 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1654
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 492 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
 QY 1655 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1714
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 552 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 611
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 10 612 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
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 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 10 672 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 731

RESULT 14

BQ109287

LOCUS

DEFINITION

BQ109287 666 bp mRNA linear EST LOC 4082
 IMAGE:5054693 5' mRNA sequence

ACCESSION

BQ109287.1

VERSION

GI:20158941

KEYWORDS

EST

SOURCE

Mus musculus

ORGANISM

house mouse

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurostomatia; Muridae; Mus;

1 (bases 1 to 666)

Plaque, C.K.

The I.M.A.G.E. Consortium

responsible for verification

other ESTs: BL147297

Contact: Plaque, C.K.

The I.M.A.G.E. Consortium

Lawrence Livermore National Laboratory

Livermore, CA, USA

Email: help@imga.llnl.gov

This read has been verified (found to hit its original self in the

correct orientation), as part of the I.M.A.G.E. Consortium quality

control effort. High quality sequence is defined as having 100 or

more base pairs with a phased quality value of 20 or greater, where

a sliding window of 4 base pairs with a phased quality value of 15

or greater marks the beginning and end of the sequence. For

information on obtaining this clone, please contact
 info@imga.llnl.gov.

Plate: 14AM1148 row: j column: 6

Seq primer: ml3rpl

High quality sequence step: 666.

Location/Qualifiers

FEATURES

Source

1..666

/organism="Mus musculus"

/strain="IMV/N"

/db_xref="taxon:10090"

/db_xref="IMAGE:5054693"

/clone_lib="NCLCAP_149"

/lab_host="DH10B (TI phase resistant)"

/vector="pGAP11 (TI phase resistant)"

Site_2: Salt; Cloned unidirectionally. primer: ml3rpl d1.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCLCAP library."

BASE COUNT 144 a 185 c 146 g 190 t 1 others

ORIGIN

Quality Match

25.24; Score 459; BB 14; Length 666;

Best Local Similarity 81.64; Pred. No. 2.8e-118;

Matches 512; Conservative 6; Mismatches 121; Indels 1; Gaps 1;

QY 1117 TACAAAGTGTGAAACCAATAATTTGTATTCAACCTCCGACGACGCTATGCAATTCAT 1176

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

DL 2 TACAAATATCAAAATATTTGTGTCAATTCGACGACGCTATGCAATTCAT 61

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 1177 GTTATATTTCTTTTATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1236

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

DB 62 GTTATATTTCTTTTATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 121

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 1237 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1296

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

DB 122 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 181

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 1297 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1356

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

DB 182 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 241

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 1357 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1416

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

DB 242 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 301

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 1417 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1476

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

DB 392 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 451

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 1477 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1536

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DB 462 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 521

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QY 1537 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1596

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

DB 422 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 481

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QY 1597 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1656

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DB 482 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 541

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QY 1657 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1716

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DB 542 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 601

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 1716 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1775

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

DB 602 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 661

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 1776 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 1835

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DB 662 TCGGTTCGACGACAAATATGCGAGCTTCACTTTCTTCTTCTTCTTCTTCTTCTTCT 721

1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

440 ATGCTGGGCTGTCGTCATGCTGCTACACAGCGGCTACATCTTTTATAATCATGCTG 499
 445 ATCTTAGGCTGTCGTCATGCTGCTACACAGCGGCTACATCTTTTATAATCATGCTG 404
 500 CTGCTGCTGGCAATATATGCTACGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559
 505 CTGCTGCTGGCAATATATGCTACGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 414
 560 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 619
 565 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 524
 620 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 679
 625 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 584
 680 ATTAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739
 685 ATTAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 644
 740 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 799
 745 GAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 704
 800 CTGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
 805 CTGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 764
 860 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 919
 865 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824
 920 GTTCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 979
 925 GTTCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 884
 980 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039
 985 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944
 1040 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1099
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 1100 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1159
 1105 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1064
 1160 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1219
 1165 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1124
 1220 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1279
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 1640 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1604
 1645 ATGCTGCTGGTAAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1554
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RESULT

US-09-789-919-65

Sequence 65, Application: US/09-789-919

Patent No. US/09-789-919

GENERAL INFORMATION:

APPLICANT: Lemis, Inc.

TITLE OF INVENTION: METHOD FOR

TITLE OF INVENTION: METHOD FOR

FILE REFERENCE: 4279-1-005

CURRENT FILING DATE: 2001-02-21

NUMBER OF SEQ. IN SET: 65

SOFTWARE: Patenting Ver. 2.0

SEQ. ID NO. 65

LENGTH: 4859

ORGANISM: Mus musculus

US-09-789-919-65

QUALITY MATCH: 65.5%

Best Local Similarity: 81.9%

Matching: 100%

Mismatched: 0%

Gaps: 0%

Gaps: 0%

Gaps: 0%

Gaps: 0%

Gaps: 0%

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Gaps: 0%

Gaps: 0%

Gaps: 0%

Gaps: 0%

Gaps: 0%

Gaps: 0%

Best local Similarity 1.00%; Prod. No. 1.24-097

Matches 6; Conservative 242; Mismatches 149; Indels 0; Gaps 0.

```

QY 4 TTTAAATAGTAAAGAAATGACACAGCTGATATAATTAATTAAGAAAGATGCTC 64
J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J
DB 1457 TACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1478
QY 64 TGAATATATATATATATATATATATATATATATATATATATATATATAT 124
J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J
DB 1377 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1418
QY 124 AAGAGGTTGTGTGATGAGAAAGAAAGAGCTGAGAGTGAATATGAGAACTGAG 184
J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J
DB 1217 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1258
QY 184 AATATGTCATATGACCAAGATGATGAGAGAGTGTGAGAAAGTCTCTATAGATAGT 243
J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J
DB 1257 TTTTTRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1198
QY 244 CATATATATATATATATATATATATATATATATATATATATATATAT 304
J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J
DB 1197 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1148
QY 304 TGAAGAGTAAAGAAATGAGAAAGAAATTTTGAAGAAAGAAAGTGTGAGATATG 364
J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J
DB 1137 PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 1078
QY 364 TATATGAACACATCC 479
J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J J
DB 1077 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1062

```

RESULT 2

US-08-242-464-14

Sequence 14, Application US/08/242-464

Patent No. 5670367

GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHREIBER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT POWDERX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Hardner

STREET: 1800 diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22312-0297

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compat file

OPERATING SYSTEM: PC-95/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/242-464

FILING DATE:

CLASSIFICATION: 4.5

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,413

FILING DATE:

APPLICATION NUMBER: EP 91 114 360.6

FILING DATE: 26-AUG-1991

AUTOREY/ABSTRACT: YES/NO: N

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

PROPRIETARY/WORK NUMBER: 90122314-0297

TELEPHONE: (703) 846-9300

TELEFAX: (703) 843-4100

TELEX: 999149

INFORMATION: YES/NO: N

SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs

TYPE: nucleic acid

STRATEGY: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

CLONE: p12apt-Fls

US-08-232-463-14

Query Match: 3.08; Score 55.2; DB 1; Length 7218;

Best local Similarity: 4.5%; Prod. No. 24-097;

Matches 18; Conservative 221; Mismatches 159; Indels 0; Gaps 0;

QY 1274 TGTATGATGAGT 1168

DB 1044 TGTATGATGAGT 1168

QY 1344 TATATGATGAGT 1308

DB 1104 TGTATGATGAGT 1168

QY 1344 TGTATGATGAGT 1308

DB 1164 TGTATGATGAGT 1228

QY 1454 TGTATGATGAGT 1518

DB 1224 TGTATGATGAGT 1288

QY 1514 TGTATGATGAGT 1578

DB 1284 TGTATGATGAGT 1648

QY 1574 TGTATGATGAGT 1638

DB 1344 TGTATGATGAGT 1408

QY 1634 TGTATGATGAGT 1671

DB 1604 TGTATGATGAGT 1441

RESULT 4

US 08 484-101B 41

Sequence 11, Application US/08/484101B

Patent No. 5624868

GENERAL INFORMATION:

APPLICANT: California Institute of Technology

TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO

TITLE OF INVENTION: ETHYLENE

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard F. Treacartin

STREET: 5400 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,101B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 800

REMARKS: APPLICATION DATA:

APPLICATION NUMBER: 50122314-0297

FILING DATE: 01-JUL-1994

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/086,555

FILING DATE: 01-JUL-1994


```

? Sequence 1780, Application US/09134001C
? Patent No. 6340036
? GENERAL INFORMATION:
? APPLICANT: US/09134001C-Stamm et al
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
? FILE REFERENCE: GTC-001
? CURRENT APPLICATION NUMBER: US/09/044,051C
? PRIOR FILING DATE: 1998-08-13
? PRIOR APPLICATION NUMBER: US 60/664,964
? PRIOR FILING DATE: 1997-11-08
? PRIOR APPLICATION NUMBER: US 60/655,775
? NUMBER OF SEQ ID NOS: 5572
? SEQ ID NO 1780
? LENGTH: 616
? TYPE: DNA
? ORGANISM: Staphylococcus epidermidis
? US-09-134-001C-1780

Query Match
Best local similarity: 96.4%, P-adj. No. 0.07, 51; Indels 0; Gaps 0;
Matches 66; Conservation 0; Mismatches 51;

QY 787 AATTATCTTCACATTCGTCGCTTAAATTTAGGTTATCTTGGCTATACCAAGGATT 846
      ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 298 AATGATGAGGCTGACAGCTGCTTTCAGAAATTTACCAATTTACCAACCAAGAAAT 357
      ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 847 TCTCTTAGTCAAGGCTGCTTTCAGAAATTTAGGTTATCTTGGCTATACCAAGGATT 903
      ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 358 AICTTTAGTCCAGGAGACTTACCTATGATGCTGATTTAGAAACAATTAGATAT 414
      ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-149-476-216/C
? Sequence 216, Application US/09149476
? Patent No. 6420526
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: 149 human secreted proteins
? FILE REFERENCE: P2802P1
? CURRENT APPLICATION NUMBER: US/09/149,476
? PRIOR FILING DATE: 1998-09-08
? EARLIER APPLICATION NUMBER: PCT/US98/04493
? EARLIER FILING DATE: 1998-03-06
? EARLIER APPLICATION NUMBER: 95/040,152
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/040,333
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/038,621
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/040,620
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/040,354
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/040,336
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/040,163
? EARLIER FILING DATE: 1997-03-07
? EARLIER APPLICATION NUMBER: 60/047,800
? EARLIER FILING DATE: 1997-05-23
? EARLIER APPLICATION NUMBER: 60/047,615
? EARLIER FILING DATE: 1997-05-23
? EARLIER APPLICATION NUMBER: 60/047,597
? EARLIER FILING DATE: 1997-05-23
? EARLIER APPLICATION NUMBER: 60/047,502
? EARLIER FILING DATE: 1997-05-23
? EARLIER APPLICATION NUMBER: 60/047,033
? EARLIER FILING DATE: 1997-05-23
? EARLIER APPLICATION NUMBER: 60/047,583
? EARLIER FILING DATE: 1997-05-23
? EARLIER APPLICATION NUMBER: 60/047,617
? EARLIER FILING DATE: 1997-05-23
? EARLIER APPLICATION NUMBER: 60/056,882

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 Db 1412 TGGNTAYYINATGGAYYINTTYMGNTGCAAPCTNTTYCAYGSHACNATHGGAARGAYA 1471
 QY 1635 TTATCTCTCACCAGCTTTTATGCTTAAAGCTTGTCAGAGAAAGAACTTLAGGICAGCCG 1694
 Db 1472 HTTAYAYCARGARTGGTGAAYYINMGNMGNYNINAAATAYCARH3NYTNTGYCCNGCNA 1531
 QY 1695 AAAAGGTCCGGGCTTTTAAATTTCCCTTGCGTTGGGATATCTTCATGATTGGAAGCATGG 1754
 Db 1532 THCCNCAYWSNGARGARGAYITTYGAYCCNGGNGCNAATTYCAVTTYWSNCGNGGTNC 1591
 QY 1755 CACTCATTAATACTGACGGATTTAIGATCCTCCGAAATTCGCAAGCATCAGIAA 1807
 Db 1592 CNTAYATHHCRNGNTAYITTYTNW5NYTNG.NYTNCAITTYCARITTYCAVGAR 1644

Search completed: January 4, 2003, 15:11:32
 Job time : 246.153 secs



ER W:200106146.AZ.
 XX
 PD 29-NOV-2001.
 XX
 PF 17-MAY-2001: 2901W-0216019.
 XX
 PR 19 MAY 2003, 230303Z 20020401.
 XX
 FA (MILL.) MILDENHURF PHARM INC.
 XX
 FT CURTIS RAE;
 XX
 FI
 DR KPI: 2002-084084/11
 DR P-PSDB: AMB09219.
 XX
 PI New membrane transporter protein (referred to as 57256 and 58289),
 PI useful for diagnosing, treating disorders e.g. Alzheimer's disease
 PI mania, obsessive-compulsive disorder, anxiety and diabetes.
 XX
 PS Claim 1: Fig 4: 14pp; English.
 XX
 CC The sequence encodes human membrane transporter protein 58289. The
 CC invention relates to novel isolated membrane transporter protein (s) of the
 CC polypeptides, (referred to as 57256 and 58289). The polypeptides of the
 CC invention have neurotropic, neuroprotective, anti-Alzheimer's disease,
 CC anticonvulsant, neuroleptic, antidepressant, anxiolytic, tranquilizer,
 CC antimutagenic, anorectic, antihypertensive, vasorelaxant, cardiac,
 CC antitumoral, antiarrhythmic, cytostatic, antitumor, and immunostimulant
 CC activity. The polypeptides and polypeptide fragments in gene
 CC therapy, and act as modulators of the protein of nucleic acid, and as
 CC transcription and/or translation inhibitors. Both the polypeptide and
 CC polypeptide are useful as modulation agents in regulating cellular
 CC process e.g. cellular proliferation, growth, differentiation, or
 CC mutation, which is useful in treatment and diagnosis of transporter
 CC associated disorders. These disorders include central nervous system
 CC (CNS) disorders, autoimmune function disorders, learning or memory
 CC disorders, bipolar affective neurological disorders, cardiac related
 CC disorders, cancer, tumor angiogenesis and metastasis, skeletal
 CC dysplasia, hepatic disorders, hematopoietic and/or metabolic disorders,
 CC disorders, hormonal disorders, and immune disorders. The polypeptides and
 CC polynucleotides, and homologues of the polynucleotides and antibodies,
 CC are useful for screening assays, predictive medicine (e.g. diagnostic
 CC assays, prognostic assays, monitoring clinical trials, and
 CC pharmacogenetics) and treatment (e.g. therapeutic and prophylactic).
 XX
 SQ Sequence 3767 bp: 1157 A: 713 C: 690 G: 1207 T: 0 other:

Query Match: 98.1% Score 1787.2; DB 24; Length 3767;
 Best Local Similarity: 99.6% Prod No:
 Matches 1792; Conservative: 9; Mismatches: 8; Indels: 0; Gaps: 0;

QY 23 GCTGTCACAGAACTGGATATAAATAATTAAGAAATAGATGTTCTGAAATATTAACACAAAGTG R2
 DB 18 GCTGTCACAGAACTGGATATAAATAATTAAGAAATAGATGTTCTGAAATATTAACACAAAGTG 77
 QY 83 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 142
 DB 78 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 147
 QY 144 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 202
 DB 148 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 197
 QY 204 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 262
 DB 198 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 257
 QY 264 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 322
 DB 258 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 317
 QY 324 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 382

118 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 437
 QY 484 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 442
 DB 178 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 437
 QY 444 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 502
 DB 448 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 497
 QY 504 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 562
 DB 498 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 557
 QY 564 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 622
 DB 568 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 617
 QY 624 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 682
 DB 618 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 677
 QY 684 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 742
 DB 676 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 737
 QY 744 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 802
 DB 738 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 797
 QY 804 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 862
 DB 798 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 857
 QY 864 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 922
 DB 858 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 917
 QY 924 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 982
 DB 918 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 977
 QY 984 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1042
 DB 978 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1037
 QY 1044 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1102
 DB 1038 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1097
 QY 1104 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1162
 DB 1098 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1157
 QY 1164 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1222
 DB 1158 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1217
 QY 1224 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1282
 DB 1218 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1277
 QY 1284 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1342
 DB 1278 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1337
 QY 1344 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1402
 DB 1338 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1397
 QY 1404 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1462
 DB 1398 AAGAAATCTTAAGATGAAATGAATATTAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1457

PI full length cDNAs defined in the specification, and for the detection
PI and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -

PS Claim 1: SEQ ID 687: 2547bp - 97.6% English.

XX the present invention described below relate to a method for detecting a
CC full-length cDNAs defined in the specification, where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in an in vitro therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full length cDNAs, the primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialized methods. AAB2166 to AAB2168 and
CC AAB1463 to AAB1874 represent human genes. In the present invention, AAB2166
CC AAB2167 and AAB2168 represent human genes. AAB2166, AAB2167 and
CC AAB2168 represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX Sequences 618 bp: 294 A; 176 G; 24 C; 220 T; 2 other.

Query Match	47.5%	Score 682.4	DB 22: Length 918;
Best Local Similarity	96.0%	Pred. No. 26 190	
Matches 720;	Conservative 0;	Mismatches 28;	Indels 2;
Ops 2;			
QY 41	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	100	
DB 153	ACAGAAAAAAGAAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	212	
QY 101	AGTACAT	160	
DB 21	AGTACAT	272	
QY 161	CAAAATGAT	220	
DB 273	CAAAATGAT	322	
QY 221	AGAGAAAGAT	280	
DB 433	AGAGAAAGAT	392	
QY 281	AGTAAAT	340	
DB 493	AGTAAAT	452	
QY 441	AAAAAAGATGAT	400	
DB 453	AAAAAAGATGAT	512	
QY 401	TCTTAT	460	
DB 513	TCTTAT	572	
QY 461	ATGAGTAT	520	
DB 573	ATGAGTAT	642	
QY 521	ATGAGTAT	580	
DB 603	ATGAGTAT	642	
QY 581	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	610	
DB 613	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	610	

DB 633	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	702
QY 640	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	699
DB 753	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	812
QY 760	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	769
DB 813	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	871
QY 760	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	789
DB 872	AAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA	901

RESULT 7

AAAL21901

AAAL21901 standard; cDNA: 678 bp.

XX AAAL21901;

XX 07-08-2001 (first entry)

XX Human breast cancer expressed polynucleotide 1458.

XX Human breast cancer, cell marker; cytostatic; SS.

XX Homo Sapiens.

XX W228371626 A2.

XX 19-jun-2001.

XX 10 JAN 2001; 2001W0-US00798.

XX 14 JAN 2000; 2000US-0176077.

XX 14 JAN 2000; 2000US-0189167.

XX 24 MAR 2000; 2000US-0192049.

XX 24 MAR 2000; 2000US-0193480.

XX 15 MAY 2000; 2000US-0205240.

XX 09 JUN 2000; 2000US-0211315.

XX 25 JUL 2000; 2000US-0220534.

XX (M115.) MULTIPERSON PREDICTIVE MEDICINE INC.

XX Li: He J, X. Y, Wang Y, Shoumiao K.

XX WP: 2001 451356/48.

XX New peptide useful as a marker for the diagnosis of breast cancer

XX Claim 1; Page 2574; 3695pp; English.

XX The invention relates to human breast cancer expressed polynucleotides
XX (AAAL21901) and methods of assessing whether a patient is
XX afflicted with breast cancer by examining the correlation between the
XX expression of certain markers and the cancerous state of breast cells.
XX The polynucleotides and encoded polypeptides are potential markers for
XX detecting, diagnosing, monitoring, characterizing treatment and
XX potentially preventing breast cancer. The polynucleotides and encoded
XX polypeptides are also useful for isolating compounds with cytostatic
XX activity.

XX Sequence 678 bp: 219 A; 129 C; 168 G; 171 T; 0 other;

XX Query Match 41.7%; Score 578.2; DB 22; Length 678;

XX Best Local Similarity 95.9%; Pred. No. 8,96-160;

XX Matches 720; Conservative 0; Mismatches 28; Indels 2; Ops 2;

XX 102 CAAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA

XX 102 CAAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA

XX 102 CAAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA

XX 102 CAAATTAATTAAGAAAGATGTTTGAATATTAAGTAAAGTGAAGAAATTAAGTGAAGTAA

QY 1490 TTTGGGAAAAGAGCGCTTCAGTGGATACAGATTTTCTGCAATGTAATGCTGCTGCTATATGCA 1549
 DQ 1440 TGTGCAACAAAACATTTAGCTTGTGGTCAATATATATATATATATATATATATATATATATAT 1499
 QY 1550 CTAAATAAAGCTTCTGCTAT 1609
 DQ 1500 TTACCAATTTAGCTGCTAT 1559
 QY 1610 GTTCTCTGCGCAATGCTGATTTTATTTATCTGCGCAGCTTTTATATATATATATATATATAT 1669
 DQ 1560 GCACTGCAAGCTGATGCTGATTTTATTTATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1619
 QY 1670 AATAAATAATTTAT 1729
 DQ 1620 AATAAATAATTTAT 1679
 QY 1730 ATATCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1739
 DQ 1680 ATATCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1739

RESULT 14

AAL14373

AAL14373 standard: cDNA; 606 BP.

 XX AAL14374;
 AC

 XX 07-DEC-2001 (first entry)
 DQ

 XX Human breast cancer expressed polypeptide (606)
 DE

 XX Human breast cancer; cell marker; cytostatic; SS
 KW

 XX Homo sapiens.
 QS

 XX W0200151628 A2.
 PN

 XX 19-JUL-2001.
 DQ

 XX 10-JAN-2001; 2001WO US00798.
 PF

 XX 14-JAN-2000; 2000US-0174077.
 PR

 XX 14-MAR-2000; 2000US-0189167.
 PR

 XX 24-MAR-2000; 2000US-0194099.
 PR

 XX 29-MAR-2000; 2000US-0194480.
 PR

 XX 15-MAY-2000; 2000US-0205230.
 PR

 XX 09-JUN-2000; 2000US-0211315.
 PR

 XX 25-JUL-2000; 2000US-0229534.
 PR

 XX (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA

 XX Little J., Xu Y., Wang Y., Steinmann K;
 PT

 XX WPI; 2001 451856/48.
 DE

 XX New peptide useful as a marker for the diagnosis of breast cancer
 PT

 XX Claim 1; Page 12/42; 369pp; English.
 QS

XX The invention relates to human breast cancer expressed polypeptides like (AAL07544-AAL26785) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the oncogenic state of breast cells. The polypeptides and encoded polypeptides are potential markers for detecting, diagnosing and encoded polypeptides are potential markers for potentially preventing breast cancer. The polypeptides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.

XX Sequence 606 BP; 188 A; 113 C; 111 G; 188 T; 6 other;

Query Match 19.5%; Score 356; DB 22; Length 606;

Best Local Similarity 100.0%; Pred. No. 2,5e-94;

Matches 566; Conserved size 0; Mismatches 1; Indels 1; Gaps 0
 QY 1490 GTAAAT 1549
 DQ 1440 GTAAAT 1499
 QY 1550 GTAAAT 1609
 DQ 1500 GTAAAT 1559
 QY 1610 GTAAAT 1669
 DQ 1560 GTAAAT 1619
 QY 1670 GTAAAT 1729
 DQ 1620 GTAAAT 1679
 QY 1730 GTAAAT 1739
 DQ 1680 GTAAAT 1739

RESULT 15

AAL26785

AAL26785 standard: cDNA; 765 BP.

 XX AAL26786;
 AC

 XX 07-DEC-2001 (first entry)
 DQ

 XX Human breast cancer expressed polypeptide (765)
 DE

 XX Human breast cancer; cell marker; cytostatic; SS
 KW

 XX Homo sapiens.
 QS

 XX W0200151628 A2.
 PN

 XX 19-JUL-2001.
 DQ

 XX 10-JAN-2001; 2001WO US00798.
 PR

 XX 14-JAN-2000; 2000US-0174077.
 PR

 XX 14-MAR-2000; 2000US-0189167.
 PR

 XX 24-MAR-2000; 2000US-0194099.
 PR

 XX 29-MAR-2000; 2000US-0194480.
 PR

 XX 15-MAY-2000; 2000US-0205230.
 PR

 XX 09-JUN-2000; 2000US-0211315.
 PR

 XX 25-JUL-2000; 2000US-0229534.
 PR

 XX (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA

 XX Little J., Xu Y., Wang Y., Steinmann K;
 PT

 XX WPI; 2001 451856/48.
 DE

 XX New peptide useful as a marker for the diagnosis of breast cancer
 PT

 XX Claim 1; Page 28/50; 369pp; English.
 QS

XX The invention relates to human breast cancer expressed polypeptides like (AAL07544-AAL26785) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the oncogenic state of breast cells. The polypeptides and encoded polypeptides are potential markers for detecting, diagnosing and encoded polypeptides are potential markers for potentially preventing breast cancer. The polypeptides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.

CC activity.

XX Sequence 555 bp; 232 A; 156 C; 147 G; 224 T; 0 other;

Query Match 19.5%; Score 396; DB 22; Length 755;

Best Local Similarity 100.0%; Prod. No. 2-90-94;

Matches 456; Conservative 9; Mismatches 2; Indels 0;

QY 1467 GTATCAACAGATCAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 1526

DB 2 GTATCAACAGATCAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 61

QY 1527 GAAATCAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 1586

DB 62 GTATCAACAGATCAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 121

QY 1587 AATAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 1646

DB 122 AATAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 161

QY 1647 CAGTCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 1706

DB 182 CAGTCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 241

QY 1707 CTTAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 1766

DB 242 CTTAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 321

QY 1767 TGAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 1826

DB 302 TGAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 400

RESULT 14

ABN96875

DB ABN96875 standard; DNA; 560 BP.

XX

AC ABN96875;

XX

DE 10-OCT-2001 (first entry)

XX

DE Marine 7-transmembrane G-protein coupled receptor coding sequence #446.

XX

KW Marine; stromal stem cell; signalling; vasculine; 7TM-epitex;

KW 7-transmembrane G-protein coupled protein receptor; ds.

XX

OS Mus sp.

XX

FN W020010999-A1.

XX

FF 23-AUG-2001.

XX

FF 14-FEB-2001; 2001W0050470h.

XX

PR 14-FEB-2001; 2000NS 6102377.

XX

PA (IMC1-) IMCONE SYSTEMS INC.

PA (IMC1-) UNIV PRINCETON.

XX

PI Lemischka IK, Witto L, Perreira DS;

XX

GR W01; 2000-500690-267

XX

XX DNA Sequences encoding 7-transmembrane G-protein coupled protein

PI receptors characteristic of hematopoietic stem cells, useful for

XX treating leukemia.

PS Claim 1; Page 151; 176pp; English.

XX

CC The present invention relates to murine coding sequences for

XX 7-transmembrane G-protein coupled protein receptors (7TM-epitex). The

XX present sequence is one such murine 7TM-epitex coding sequence. The present

XX sequence was derived from stromal stem cells. The present sequence

CC and its corresponding protein are useful in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate 7TM-epitex expression.

CC 7TM-epitex identify specific signalling molecules, to activate an

CC effector-signalling cascade that triggers an intracellular response and

CC eventually a biological effect.

CC Sequence 560 bp; 149 A; 141 C; 126 G; 151 T; 13 other;

Query Match 18.5%; Score 337.4; DB 22; Length 560;

Best Local Similarity 84.1%; Prod. No. 7-50-89;

Matches 403; Conservative 0; Mismatches 79; Indels 5; Gaps 2;

QY 546 AATATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 1407

DB 1 AATATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 60

QY 408 TAAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 467

DB 61 TAAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 120

QY 468 ACAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 527

DB 121 ACAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 180

QY 528 GAGTCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 587

DB 181 GAGTCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 240

QY 588 TAAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 647

DB 241 TAAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 706

QY 648 ACAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 707

DB 601 ACAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 766

QY 708 TAAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 767

DB 661 TAAATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 826

QY 767 AATATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 827

DB 421 AATATCTGTTATTTCTCAAGCAAGACCTGAGTGTGATATGACATATTC 886

QY 825 AATCT 824

DB 481 AATCT 485

RESULT 15

ABN96875

DB ABN96875 standard; DNA; 2431 BP.

XX

AC ABN96875;

XX

DE 14-AUG-2002 (first entry)

XX

DE Gene #3373 used to diagnose liver cancer.

XX

KW Genco; liver cancer; ds; hepatocellular carcinoma; hepato topic;

KW Molecular Biology; Genco; 2732 bp; 1431 bp; 1431 bp; 1431 bp;

XX

OS Homo sapiens.

XX

FN W0200229104-A2.

XX

PD 11-APR 2002.

XX

XX 02-OCT-2001; 2001W0050509.

XX

PR 02-OCT-2001; 2000NS-247054P.

XX



10 855 WWTAWTAAAAATYAAATTTAAAWTAWAWA 882

Search completed: January 4, 2003, 12:30:50
Job time : 769.432 secs

[illegible]

RESULT 13
JS 09 960 352-7166/c
Sequence 7166, Application 05/09960352
Patent No. US20020137139A1

RESULT 13
 JS 09 963 352-7186/C
 Sequence 7186, Application US/99-03352
 Patent No. US20020137139A1
 GENERAL INFORMATION:
 APPLICANT: Waitreth, Wesley C.
 APPLICANT: Tao, Ningbing
 APPLICANT: Byatt, John C.
 APPLICANT: Mathialagan, Naqappan
 TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 FILE REFERENCE: MUSCLE AND FAT DEPOSITION
 FILE REFERENCE: 16511-096/337 21(10298)C
 CURRENT APPLICATION NUMBER: 09/0960352
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112

TYPE: DNA
ORGANISM: Bos taurus
GROUP INFORMATION: 113334 31 37 106565 66 64 81 84
IS-09-060-352-7186

Query Match
Best Local Similarity 46.8%; DB 10; Length 468;
Matches 112; Occurrences 9; P-values 1.57; Identities 0; Gaps

RESULT 14
 BUS-09-867-701-7175
 ; Sequence 7175, Application US/09046,7701
 ; Patent No. US2,201,322A1
 ; GENERAL INFORMATION:

RESULT 14
 US-09-867-701-7175
 ; Sequence 7175 ; Affiliation US/09667701
 ; Patient No. US-09-2013237A1
 ; GENERAL INFORMATION:

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 08:10:57, Search time 752.955 Seconds
(without alignments)
10634.887 Million cell updates/sec

Title: US-09-776-705-3_copy_15000_15500
Perfect score: 501
Sequence: 1 atgtggaattattatcat.....tgaacaaatgaggaagaaag 501

Scoring table: IDENTIFY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 reads, 807774376 residues
Total number of hits satisfying chosen parameters: 22308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST.*
1: em_estba.*
2: em_esthum.*
3: em_estlin.*
4: em_estnu.*
5: em_estov.*
6: em_estpi.*
7: em_estro.*
8: em_hic.*
9: qb_est1.*
10: qb_est2.*
11: qb_hic.*
12: qb_est3.*
13: qb_est4.*
14: qb_est5.*
15: em_estun.*
16: em_estom.*
17: qb_gss.*
18: em_gss_hum.*
19: em_gss_lin.*
20: em_gss_pln.*
21: em_gss_vit.*
22: em_gss_fun.*
23: em_gss_nam.*
24: em_gss_rus.*
25: em_gss_oth.*
26: em_gss_pro.*
27: em_gss_fod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	62	12.4	821	17	B0658662
2	56.8	11.3	1029	17	CNS012GM
3	56.6	11.3	1101	17	CNS0039C
4	55.4	11.1	1101	17	CNS00EVL
5	53.4	10.6	1632	17	CNS025K7
6	53	10.6	1101	17	CNS00EVL

7	52.8	10.5	1085	17	CNS0124K
8	52.6	10.5	616	17	B0658662
9	51.6	10.4	1029	17	CNS012GM
10	51.2	10.2	1101	17	CNS00EVL
11	50.2	10.0	1061	17	CNS015LM
12	50.2	10.0	1101	17	CNS00F07
13	49.8	9.9	549	13	B0161310
14	49.8	9.9	1184	17	CNS04F4F
15	49.6	9.9	660	13	B0286434
16	49.6	9.9	802	17	CNS01241
17	49.4	9.9	1101	17	CNS00380
18	48.8	9.7	494	13	B2251117
19	48.8	9.7	497	13	B0291605
20	48.8	9.7	545	13	B0291477
21	48.8	9.7	547	13	B0291462
22	48.8	9.7	632	13	B0291506
23	48.8	9.7	646	13	B0291635
24	48.8	9.7	672	13	B0292335
25	48.8	9.7	678	13	B0292438
26	48.8	9.7	697	13	B0294194
27	48.8	9.7	750	13	B0290938
28	48.8	9.7	753	13	B0292610
29	48.8	9.7	761	13	B0292688
30	48.8	9.7	767	13	B0290950
31	48.8	9.7	782	13	B0292204
32	48.4	9.7	684	13	B0290870
33	48.4	9.7	723	17	A0476747
34	48.4	9.7	1101	17	CNS0178E
35	48	9.6	460	13	B0291508
36	48	9.6	467	13	B0291407
37	48	9.6	515	13	B0291298
38	48	9.6	627	13	B0290067
39	48	9.6	726	13	B0292433
40	47.8	9.5	609	17	CNS023K2
41	47.4	9.5	635	13	B0291532
42	47.4	9.5	1091	17	CNS01400
43	47.4	9.5	1092	17	CNS029K7
44	47.4	9.5	1101	17	CNS00493
45	47	9.4	487	9	A0297526

ALIGNMENTS

RESULT 1
LOCUS B0658662/c
DEFINITION B0658662
ACCESSION B0658662
KEYWORDS B0658662.1 GI:18717104
SOURCE GSS.
ORGANISM Brassica oleracea.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosidae; eucosids II; Brassicales; Brassicaceae; core eudicots.
REFERENCE 1 (bases 1 to 821)
AUTHORS Tatem, C. B., Van Aken, S., Hutterback, T. and Fraser, J. M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: CHRIS TATEM
TAGLOC Medical Center, Detroit, Rockville, MD 20850, USA.
Tel: 401-848-4523
Fax: 401-848-0208
Email: c.tatem@rockefeller.edu
DNA is from a doublet haploid provided by Tom Tatem
Seq primer: TF
Class: Sheared ends.
Genetic Qualifiers
1: 821
/organism="Brassica oleracea"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db 719 ATATKAGWCKCTTTTITTTTTTWWAWAAATTTTAAAAAATAAATWAAAWAAATTTTTTT 778

QY 144 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 203

Db 779 AWAATWAAATTAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 848

QY 204 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 263

Db 839 AWAATWAAATTAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 898

QY 254 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 323

Db 899 AWAATWAAATTAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 958

QY 324 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 383

Db 959 AWAATWAAATTAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 1018

QY 384 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 443

Db 1019 AWAATWAAATTAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 1078

QY 444 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 459

Db 1079 AWAATWAAATTAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 1094

RESULT 11

CNS015LM/c

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of PAC

BACN14105 of Drosophila library from Drosophila melanogaster (fruit

fly); genomic survey sequence.

AL105604

AL105604.1 G1:5617618

SSS.

Drosophila melanogaster.

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydridea; Drosophilidae; Drosophila.

1 (bases 1 to 1061)

Genoscope.

Direct Submission

Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

Determination of this PAC-end sequence was carried out as part of a

collaboration with the European Drosophila Genome Project (PDBP) -

http://www.eugp.cba.ac.uk - this Drosophila melanogaster PAC

library (Dros PAC) was made by Alain Billaud at CERH (Centre

d'Etude de Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Richeton

and Genevieve Payan. It has been constructed in the vector

pBeloBAC11.

FEATURES

Location/Qualifiers

1..1061

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACN14105"

/clone_lib="DrosPAC"

/plasmid="pBeloBAC11"

/note="end : T7"

BASE COUNT 342 a 89 g 277 t 215 others

ORIGIN

Query Match 10 0%

Best local similarity 34.9%; Pred No. 0.79;

Matches 156; Conservative 67; Mismatches 222; Indels 2; Gaps 1;

QY 30 TTTCATATCAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 89

Db 1061 TTTTITTTTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 1002

QY 99 GATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 119

Db 1081 AWAATWAAATTAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTTAAAGTAAATTTT 942

QY 150 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 207

Db 941 TAAATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 882

QY 208 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 267

Db 881 TAAATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 822

QY 269 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 327

Db 821 TAAATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 762

QY 328 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 387

Db 761 TAAATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 702

QY 388 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 447

Db 701 TAAATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 422

QY 448 AAGATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 474

Db 641 TAAATTTTCAAGTAAATTTGAGTTCATATTTTAAAGTAAATTTTGGCAATGTCATCA 615

RESULT 12

CNS015LM/c

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence T12 end of PAC

BACN24961 of Drosophila library from Drosophila melanogaster (fruit

fly); genomic survey sequence.

AL069440

AL069440.1 G1:4949583

SSS.

Drosophila melanogaster.

Drosophila melanogaster.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydridea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

- Web : www.genoscope.cns.fr

Determination of this PAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDBP).

The BDBP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org/TheBDBP/Drosophila>

melanogaster BAC library was prepared by Kazuo Tozawa and

Aaron Mammos in Peter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCL-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDBP from the

isogenic strain Y2; cv. bw sp. the same strain used for the library

pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://www.fruitfly.org/BDBP/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BAC24961"

/clone_lib="RPCL-98"

/note="end : T12"

BASE COUNT 406 a 56 c 104 g 451 t 214 others

QY 94 TTTAAATGGCTGTGTTAGCAAAATTCACATGAGAGATGTAGACACATTAAGATTTTCA 153
 DB 1381 TAGATATTTTCGATAAATATCATCTTATCTTTTGGAGTATTCATTTGGATTGAA 1322
 QY 154 TGTAAATTTGGAGH 170
 DB 1321 TAACATGCTGAGH 1505

RESULT 5

US-10-037-598 32/6
 : Sequence 33, Application US/10037598
 : Patent No. US 6,500,571 A1
 : GENERAL INFORMATION:
 : APPLICANT: Monsanto Co
 : APPLICANT: Delaney, Xavier
 : TITLE OF INVENTION: Soybean Plants with Enhanced Yields and Methods for Breeding for
 : FILE REFERENCE: 38-2152175B
 : CURRENT AFFILIATION NUMBER: US/10037598
 : PRIOR APPLICATION NUMBER: 2002-01-04
 : PRIOR FILING DATE: 2001-01-05
 : NUMBER OF SEQ ID NOS: 37
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 33
 : LENGTH: 3141
 : TYPE: DNA
 : ORGANISM: Glycine max
 US-10-037-598-33

Query Match 7.58; Score 37.8; DB 9; Length 3141;
 Best Local Similarity 42.36; Pctd No. 11;
 Matches 99; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 QY 163 TGTGATCTCTTTTAACTGAACTTTTGGCATGTGTCAACAAATTAACGTTATCTT 222
 DB 744 TTTAATCAATTAATATCGTTCTTCTTCAATTTGTAAGCGCATAAATAAACCAT 685
 QY 223 CACCAAAATGTTGTTTAAAGAAAGGATGATGATGATGATGATGATGATGATGAT 292
 DB 684 CACCAAAATGTTGTTTAAAGAAAGGATGATGATGATGATGATGATGATGATGAT 625
 QY 283 TGTATGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 342
 DB 624 TGTATGTTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
 QY 343 ATCAAGAAATCTTTTCAAGA 363
 DB 564 TATCTCTTTCTTTTACAGA 544

RESULT 6

US-09-790-988-1
 : Sequence 17, Application US/09790988
 : Patent No. US 6,500,127 B1
 : GENERAL INFORMATION:
 : APPLICANT: SHIGENBU, SHUJI
 : APPLICANT: MALANABE, HIROMI
 : APPLICANT: HATTORI, MASAHIRA
 : APPLICANT: SAKAKI, YOSHIYUKI
 : TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
 : FILE REFERENCE: 081456/0159
 : CURRENT APPLICATION NUMBER: US/09790988
 : CURRENT FILING DATE: 2002-02-23
 : PRIOR APPLICATION NUMBER: JP2000-107160
 : PRIOR FILING DATE: 2000-04-07
 : NUMBER OF SEQ ID NOS: 7
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 1
 : LENGTH: 640681

TYPE: DNA
 ORGANISM: Buchnera sp.
 US-09-790-988-1

Query Match 7.58; Score 37.8; DB 10; Length 640681;

Best Local Similarity 50.98; Pctd No. 31;
 Matches 60; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
 QY 21 CACTGTTTACATGATGAAGTCAAGAAATATTTTAAATTCAGATTTAAATTTAA 80
 DB 2759 CATTATCAATCTGCTGCTTTTAAATTTTAAATTTTAAATTTTAAATTTAA 2788
 QY 81 TTTAAGTATGTTTAAAGTCTCTTAAAGAAATTTTAAAGAAATTTTAAAGTAT 149
 DB 2789 GATAAGTATGTTTAAAGTCTCTTAAAGAAATTTTAAAGTATTTTAAAGTAT 2848
 QY 141 CTTAAGTATTTTAAAGTCTCTTAAAGTATTTTAAAGTATTTTAAAGTATTT 197
 DB 2849 TTTTAAATTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTT 2905

RESULT 7

US-10-003-806-6
 : Sequence 6, Application US/10003806
 : Patent No. US 6,500,199 A1
 : GENERAL INFORMATION:
 : APPLICANT: Bishop, Colin E.
 : APPLICANT: Avonlink, Alexander I.
 : TITLE OF INVENTION: CAN 1 AND PDS P-1F IN MAZILLIAN INFERTILITY
 : FILE REFERENCE: 02066481/10524824
 : CURRENT APPLICATION NUMBER: 2001-11-02
 : PRIOR FILING DATE: 2001-11-02
 : PRIOR FILING DATE: 2000-11-03
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 6
 : LENGTH: 80657
 : TYPE: DNA
 : ORGANISM: Human
 US-10-003-806-6

Query Match 7.58; Score 37.4; DB 12; Length 180557;

Best Local Similarity 46.48; Pctd No. 30;
 Matches 122; Conservative 0; Mismatches 141; Indels 0; Gaps 0;
 QY 69 TTTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 128
 DB 134594 TTTTAAAGAAAGAAATCGGTATTTTAAATTAATTAATTAATTAATTAAT 134654
 QY 129 ATGTAAGACACATTAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTT 188
 DB 134654 TTTAAGAAAGAAATTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAA 134714
 QY 189 TTTGTCATGTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTT 248
 DB 134714 CTTTTCTTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTT 134774
 QY 249 TTTAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTT 308
 DB 134774 CTATTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAA 134834
 QY 200 ATTTAATTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAA 341
 DB 134834 CTTTTCTTTTAAAGTATTTTAAAGTATTTTAAAGTATTTTAAAGTATTT 134896

RESULT 8

US-10-003-806-9
 : Sequence 9, Application US/10003806
 : Patent No. US 6,500,199 A1
 : GENERAL INFORMATION:

: TITLE OF INVENTION: SAME AND METHODS OF USE

: FILE REFERENCE: SCRIPT300-3

: CURRENT APPLICATION NUMBER: US 09/794,842A

: PRIOR FILING DATE: 2001-08-24

: PRIOR APPLICATION NUMBER: US 60/227,866

: PRIOR FILING DATE: 2000-08-24

: PRIOR APPLICATION NUMBER: US 60/264,647

: PRIOR FILING DATE: 2001-01-16

: PRIOR APPLICATION NUMBER: US 60/300,111

: PRIOR FILING DATE: 2001-06-22

: NUMBER OF SEQ ID NOS: 5379

: SEQ ID NO 5027

: LENGTH: 2000

: TYPE: DNA

: ORGANISM: Arabidopsis thaliana

US-09-764-855-180

Query Match 7.2% Score 66.25 DB 9: Length 4785

: Best Local Similarity 50.4% Pred. No. 25:

Matches 89: Conservative 0: Mismatches 88: Indels 0: Gaps 0:

QY 47 AATAATTTTAAACACACATAGTTTAAATACAAATTTAAGTATGCTTTTAAAGTGGCTG 106

DB 447 ATAAAAATGAAAAATATAAATAATATTTTAAATTAATAATTAATAATATATATT 288

QY 107 TTAGTAAAAATTCAGTAAAGATGTAAAGAAATTTTCAAGTAAAAATTTGCG 166

DB 287 TAGAAAAAAATATCAAAATAAGCTGACAGTTAAAAATTTAATTTAATAATATATT 228

QY 167 AGTCTATTTTAAACGAAATCTTTTGGTATGCTGCAAAATAATTAAGCTTATCTTC 224

DB 227 TAATTTTTTTTTTCTGTTAATCTGATCAATAATTTGGAAGAAATAAATTTTCTAC 171

RESULT 15

US-09-764-855-180

: Sequence 180, Application US/09764855

: Patent No. US20020119519A1

: GENERAL INFORMATION:

: APPLICANT: Rosen et al.

: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

: FILE REFERENCE: P110

: CURRENT APPLICATION NUMBER: US/09/764-855

: PRIOR FILING DATE: 2001-01-17

: Prior application data removed - consult PALM or file wrapper

: NUMBER OF SEQ ID NOS: 534

: SOFTWARE: Patent In Ver. 2.0

: SEQ ID NO 180

: LENGTH: 4785

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-764-855-180

Query Match 7.2% Score 66.25 DB 10: Length 4785

: Best Local Similarity 51.6% Pred. No. 25:

Matches 83: Conservative 0: Mismatches 78: Indels 0: Gaps 0:

QY 258 TAAATATTTAAAGCTTGAAGTAAAGATTTAAAGTTTATATATATATATATATATATTT 417

DB 507 TAAAAATTAGACGAAAATGTAAGATCTTTAAATTAATAATTTAAGTAAATTTAAATTC 566

QY 418 TTCAAGAAAGAAATTTGAGAAATTTATCAAGAAATCTTTCAAGAGTAAATAATCATTC 477

DB 567 TGTAGAAATGAAGTTTATAGAAATTTAAAGATTTCTAGAAATTAATTTGATATATAT 626

QY 478 ATGTATCATCTAGATGATCATGAATTTTCACATTT 418

DB 627 AGAAGAGCTCTTTAAAGATGATGATTTCTGACATGT 667

Search completed: January 4, 2003, 15:42:17

Job time : 982.486 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 4, 2003, 18:57:31, Search time 167.726 seconds
(without alignments)
10282.476 Million cell updates/sec

Title: US-09-776-705-3_copy_15000_15500

Perfect score: 501

Sequence: 1 atgtgggggaattatctat.....tgacacagatggaagaaagaa 501

Scoring table: IDENTIFY_NUC
Gapop 10.0, Gapext 1.0

Searched: 318523 seqs, 1,2599157 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum seq id cutoff: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: R-Geneseq_1010024*

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1	/S1852/gcgdata/geneseq/geneseq-emb1/NA1980.DAT*	52.6	10.5	11049	24	ABL93218
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3	/S1852/gcgdata/geneseq/geneseq-emb1/NA1982.DAT*	52.6	10.5	11049	24	ABL93218
4	/S1852/gcgdata/geneseq/geneseq-emb1/NA1983.DAT*	52.6	10.5	11049	24	ABL93218
5	/S1852/gcgdata/geneseq/geneseq-emb1/NA1984.DAT*	52.6	10.5	11049	24	ABL93218
6	/S1852/gcgdata/geneseq/geneseq-emb1/NA1985.DAT*	52.6	10.5	11049	24	ABL93218
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15	/S1852/gcgdata/geneseq/geneseq-emb1/NA1994.DAT*	52.6	10.5	11049	24	ABL93218
16	/S1852/gcgdata/geneseq/geneseq-emb1/NA1995.DAT*	52.6	10.5	11049	24	ABL93218
17	/S1852/gcgdata/geneseq/geneseq-emb1/NA1996.DAT*	52.6	10.5	11049	24	ABL93218
18	/S1852/gcgdata/geneseq/geneseq-emb1/NA1997.DAT*	52.6	10.5	11049	24	ABL93218
19	/S1852/gcgdata/geneseq/geneseq-emb1/NA1998.DAT*	52.6	10.5	11049	24	ABL93218
20	/S1852/gcgdata/geneseq/geneseq-emb1/NA1999.DAT*	52.6	10.5	11049	24	ABL93218
21	/S1852/gcgdata/geneseq/geneseq-emb1/NA2000.DAT*	52.6	10.5	11049	24	ABL93218
22	/S1852/gcgdata/geneseq/geneseq-emb1/NA2001.DAT*	52.6	10.5	11049	24	ABL93218
23	/S1852/gcgdata/geneseq/geneseq-emb1/NA2002.DAT*	52.6	10.5	11049	24	ABL93218
24	/S1852/gcgdata/geneseq/geneseq-emb1/NA2003.DAT*	52.6	10.5	11049	24	ABL93218

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52.6	10.5	11049	24	ABL93218	Chemically treated
2	52.6	10.5	11049	24	ABL93218	Human polynucleotide
3	52.6	10.5	11049	24	ABL93218	Human immune syste
4	48.2	9.6	6077	24	ABL34246	Human immune syste
5	45.4	9.1	14924	24	ABL254322	Chemically treated
6	45.8	9.1	14924	24	ABL30225	Human immune syste
7	45.6	9.1	8467	24	ABL32108	Human immune syste
8	45.6	9.1	11036	22	AAS45411	Chemically pretrea
9	45.6	9.1	11036	24	ABK38264	DNA transcription

10	45.4	9.1	5195	24	ABL33597	Human immune syste
11	46.2	9.0	3492	22	AAS4452	S. typhimurium
12	44.4	8.9	16602	24	ABN80068	Human chemically m
13	44.4	8.9	16602	24	ABN80068	Human immune syste
14	44.1	8.9	17444	22	AAS40666	Tumour suppressor
15	44.2	8.8	15161	24	ABL70458	Chemically treated
16	44.2	8.8	15161	24	ABL70458	Human immune syste
17	44	8.8	7644	24	AAS4423	Human acute regulat
18	44	8.8	7644	24	ABL32530	Human immune syste
19	43.8	8.7	18594	24	ABL34026	Human metastasis a
20	43.6	8.7	6668	22	AAS4423	Tumour suppressor
21	43.6	8.7	6668	24	ABN80163	Human chemically m
22	43.6	8.7	6668	24	ABL32119	Human immune syste
23	43.6	8.7	18357	24	ABQ67083	Human acute regulat
24	43.2	8.6	61520	22	AAS45787	Tumour suppressor
25	43	8.6	6219	24	ABL32867	Human immune syste
26	43	8.6	6219	24	AAS63325	Chemically pretrea
27	43	8.6	6219	24	AAS63325	Human immune syste
28	43	8.6	16633	22	ABN79985	Human chemically m
29	43	8.6	16633	22	AAS63325	Human immune syste
30	42.8	8.5	8197	24	ABL70543	Chemically treated
31	42.8	8.5	8197	24	ABL70543	Human metastasis a
32	42.6	8.5	5984	24	ABQ66964	Human immune syste
33	42.6	8.5	5984	24	ABQ66964	Human immunorepres
34	42.6	8.5	7851	24	ABL33761	Human immune syste
35	42.4	8.5	10988	24	ABL70190	Chemically treated
36	42.4	8.5	10988	24	AAS61157	Human acute regulat
37	42.4	8.5	10988	24	ABK31284	Signal transductio
38	42.2	8.4	5927	24	ABL34235	Human immune syste
39	42	8.4	5927	24	ABL34235	Chemically treated
40	42	8.4	5927	24	ABL34235	Human immune syste
41	42	8.4	5927	24	ABL34235	Chemically treated
42	41.8	8.3	7456	24	ABQ44942	Human acute regulat
43	41.8	8.3	7456	24	ABQ44942	Human immune syste
44	41.8	8.3	7456	24	ABQ44942	Chemically treated
45	41.8	8.3	7456	24	ABQ44942	Human immune syste

ALTERNATES

ABN80163
D ABL92219 standard DNA: 11049 BP.

ABN80163

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ABN80163


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0Y 250 GCGATCGATAAATATTTATAGTTGTAAGGCAAAAATGGTAAAGCTATGTAATGAAGAATATATA 309
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DR 515 TTCTGGTTCCTGATTTAATATATATATATATATATATATATATATATATATATATATATAT 566
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
0Y 310 TTTATTTT 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DR 455 TCGATTC 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: January 4, 2003, 15:13:01
 Job time : 79,9648 secs

[illegible]


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1  TITLE OF INVENTION: In Vitro Transposition of Artificial
2  TITLE OF INVENTION: Transposons
3  NUMBER OF SEQUENCES: 7
4  CORRESPONDENCE ADDRESS:
5  ADDRESS: Bantec, Inc., 4000 MacKay and Bennett
6  STREET: 1001 G Street, N.W.
7  CITY: Washington
8  STATE: D.C.
9  COUNTRY: U.S.A.
10 ZIP: 20001
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC DOS/MS-DOS
15 SOFTWARE: Patent in Release #1.0, Version #1.25
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/22/204,675
18 FILING DATE: 02-MAR-1994
19 CLASSIFICATION: 435
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Kadin, Sarah A.
22 REGISTRATION NUMBER: 42,141
23 REFERENCE/CHECK NUMBER: 01107,45601
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 202,508,9100
26 TELEFAX: 202,508,9299
27 TELEX: 197439 BMBB UI
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 4164 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: double
33 TOPOLOGY: circular
34 MOLECULE TYPE: DNA (genomic)
35 HYPOTHETICAL: NO
36 ANTI-SENSE: NO
37 IMMEDIATE SOURCE:
38 CLONE: PAT 1
39 US-08-204-675 1

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Query Match      7.28; Score 46; DB 1; Length 4164;
Best Local Similarity 56.98; Prod. No. 3.9;
Matches 66; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 419 ATGTTAGTATATATATCTTATCTGTAGTCATGCAAAATCTTAACTGAAGCTACATTGA 478
    111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 4354 AGGTATATATATATATATATATATATATATATATATATATATATATATATATAT 4915
    111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
QY 479 TTTTATTTTTTAAATGCTGATTTTCTTCTGCAATGCAAAAGCATTTATATAT 444
    111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 4916 TGTGAAATTTTAAAGCTTTGTTTATTTTCTTCTGCAATGCAAAAGCATTTATAT 3971
    111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

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Search completed: January 4, 2003, 15:14:16
 Job time: 38.9648 secs

Tue Jan 7 18:16:08 2003

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